POPULATION STRUCTURE AND GENE FLOW BIAS AMONG ANADROMOUS AND RESIDENT *ONCORHYNCHUS MYKISS*

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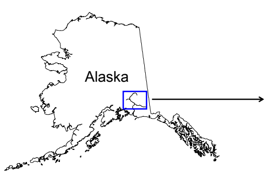
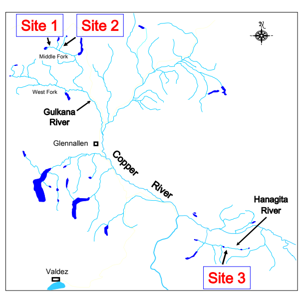
Abstract

We used 13 microsatellite loci to test for reproductive isolation and patterns of gene flow within and among sympatric anadromous (steelhead) and nonanadromous (resident) rainbow trout (*Oncorhynchus mykiss*) from the Copper River drainage in Alaska (Fig. 1). Five putative populations were sampled: sympatric steelhead and resident rainbow trout from two tributaries of the middle fork Gulkana River (Sites 1, 2) and steelhead from the Hanagita River (Site 3). Evidence of genetic differentiation among the sympatric life history types was weak (F_{ST} < 0.003) and not significant. Geographic location, not migratory type, appears to be the major determinant of population structure in Copper River *O. mykiss*. An examination of individual genotypes suggests that the rate of gene flow (straying) between sites 1 and 2 is greater for resident rainbow trout than for steelhead. These results imply that resident rainbow trout play an important role in maintaining genetic diversity of Copper River *O. mykiss*.

Introduction

Rainbow trout (*Oncorhynchus mykiss*) in western North America exhibit anadromous (steelhead) and nonanadromous (resident) migratory types that often occur in sympatry as far north as the Copper River in Alaska. Although selection pressures are likely to be very different for both forms, genetic studies have generally failed to find evidence for reproductive isolation between sympatric resident rainbow trout and steelhead. The lack of genetic support for population structure has had a major impact on conservation efforts in the northwestern U.S.A. where resident rainbow trout are now grouped with steelhead when evaluating the status of steelhead pursuant to the Endangered Species Act.





Location	Migratory Type	Code	N
Site 1	Steelhead	T1	54
	RBT	R1	67
Site 2	Steelhead	T2	55
	RBT	R2	55
Site 3	Steelhead	T3	55

Figure 1. Sample locations, population codes, and sample size.

Objectives

Using 13 variable microsatellite loci, our primary objectives are to:

1. Compare the influence of migratory type and geographic location on population structure of Copper River *O. mykiss*.

2. Evaluate the relative influence of the two migratory types on the spatial population structure of Copper River *O. mykiss*.

Site 3 – Hanagita River

Hanagita River steelhead

Methods

Sample collection

- Sympatric steelhead and resident rainbow trout were sampled from two tributaries of the Gulkana River (Fig. 1).
- Steelhead were sampled from the Hanagita River.
- Four distinguishing features were used to identify steelhead and resident rainbow trout (Fig. 2).
- Steelhead were generally larger than resident rainbow trout (Fig. 3).

Rainbow Trout

Steelhead

Rainbow Trout	Distinguishing features	Steelhead
High	1. Density of spotting	Low
Yes	2. Spots below lateral line	Few or none
Gray/white	3. Abdominal coloration	Red/gray
None	4. Sea lice scarring near anal fin insertion	Common

Figure 2. Features used to distinguish steelhead and resident rainbow trout.

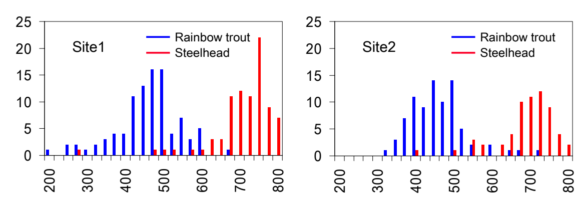


Figure 3. Length frequency histograms for steelhead and resident rainbow trout.

Data analysis

Objective 1

- Estimates of the parameter F_{ST} were computed for all population pairs to compare the influence of migratory type versus geographic location on population structure.

Objective 2:

- The program Structure (Pritchard et al. 2000) was used to estimate the population ancestry of each individual and detect immigrants among the steelhead and resident rainbow trout from sites 1 and 2.

Results

Objective 1

- Sympatric steelhead and resident rainbow trout are not distinct (Fig. 4, oval 1).
- Steelhead and resident rainbow trout from sites 1 and 2 are distinct (Fig. 4, oval 2).
- The greatest degree of genetic differentiation is seen when steelhead from site 3 are compared to steelhead and resident rainbow trout from sites 1 and 2 (Fig. 4, oval 3).

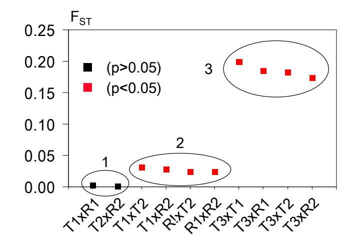


Figure 4. Estimates of F_{ST} for all population pairs. Red squares denote statistically significant genetic differentiation based on a G-test of genotypic frequency homogeneity.

Objective 2

- The proportion of ancestry (Fig. 5) from sites 1 and 2 is more variable for resident rainbow trout (R1, R2) than for steelhead (T1, T2).
- In general, steelhead from sites 1 and 2 are closer to the expected value of proportion of ancestry.
- 6 resident rainbow trout and 3 steelhead have a significant probability of being immigrants or having immigrant ancestry.

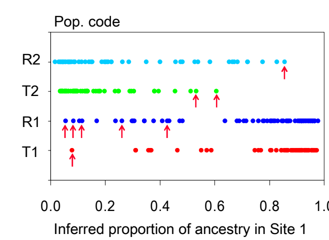


Figure 5. Inferred proportion of ancestry in site 1 for individuals from sites 1 and 2. The expectation for individuals from site 1 (T1, R1) and 2 (T2, R2) are 1.0 and 0.0 respectively. Red arrows denote individuals with a significant probability of being an immigrant or having immigrant ancestry.

Conclusions

- Classic population-based analysis suggests geographic location, not migratory type, is the major determinant of population structure in Copper River *O. mykiss*.
- Individual-based analysis suggests the rate of gene flow between the two population complexes of steelhead and resident rainbow trout is greater for resident rainbow trout than for steelhead.
- These results underscore the importance of conserving both migratory types within the Copper River.